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**Supplementary information**

**Figure S4.** **DNA sequence of recombinant gene VP1EBFP2H6 used in the study.** Translate tool from Expasy was used to obtain corresponding amino acid sequence. Clustalw was run to align amino acid sequence of GFP and EBFP2. Swiss Model was used to display 3D structure of EBFP2 protein.

>E4PL4-VP1EBFP2H6

ATGGAAACCACCACCACCGGTGAAAGCGCAGATCCGGTTACCACCACAGTTGAAAATTATGGTGGTGAAACCCAGGTTCAGCGTCGTCATCATACCGATGTTGCATTTGTTCTGGATCGTTTTGTTAAAGTTACCGTGAGCGATAATCAGCATACCCTGGATGTTATGCAGGCCCATAAAGATAATATTGTTGATGCACTGCTGCGTGCAGCAACCTATTATTTCAGCGATCTGGAAATTGCAGTTACCCATACCGGTAAACTGACCTGGGTTCCGAATGGTGCACCGGTTAGCGCACTGAATAATACCACCAATCCGACCGCATATCATAAAGGTCCGGTGACCCGTCTGGCACTGCCGTATACCGCACCGCATCGTGTTCTGGCAACCGCATATACCGGTACAACCACCTATACCGCAAGCGCACGTGGTGATCTGGCACATCTGACCACCACCCATGCACGTCATCTGCCGACCAGCTTTAACTTTGGTGCAGTTAAAGCAGAAACCATTACCGAACTGCTGGTTCGTATGAAACGTGCAGAACTGTATTGTCCGCGTCCGATTCTGCCGATTCAGCCGACCGGTGATCGTCATAAACAGCCGCTGGTTGCACCGGCAAAACAGCTGCTGGGTATTCCGAGCAAAGGTGAAGAACTGTTTACAGGTGTTGTGCCGATTCTGGTTGAACTGGATGGTGATGTTAATGGCCACAAATTTTCAGTTCGTGGTGAAGGCGAAGGTGATGCAACCAATGGCAAACTGACCCTGAAATTTATCTGTACCACAGGTAAACTGCCGGTTCCGTGGCCGACCCTGGTGACCACCCTGAGTCATGGTGTTCAGTGTTTTGCACGTTATCCGGATCACATGAAACAGCACGATTTTTTCAAAAGCGCAATGCCGGAAGGTTATGTTCAAGAACGTACCATCTTCTTCAAAGATGATGGCACCTATAAAACCCGTGCCGAAGTTAAATTTGAAGGTGATACCCTGGTTAACCGCATTGAACTGAAAGGTGTGGATTTTAAAGAGGATGGTAATATCCTGGGCCACAAACTGGAATATAATTTCAACAGCCACAACATCTATATCATGGCCGTGAAACAGAAAAACGGCATCAAAGTGAATTTCAAAATCCGCCATAATGTGGAAGATGGTTCAGTTCAGCTGGCAGATCATTATCAGCAGAATACCCCGATTGGTGATGGTCCGGTTCTGCTGCCGGATAGCCATTATCTGAGCACCCAGAGCGTTCTGAGCAAAGATCCGAATGAAAAACGTGATCACATGGTGCTGCTGGAATTTCGTACCGCAGCAGGTATTACCCTGGGTATGGATGAACTGTATAAACATCATCACCATCATCATTAA

<https://web.expasy.org/translate/>

METTTTGESA DPVTTTVENY GGETQVQRRH HTDVAFVLDR FVKVTVSDNQ HTLDVMQAHK

 DNIVDALLRA ATYYFSDLEI AVTHTGKLTW VPNGAPVSAL NNTTNPTAYH KGPVTRLALP

 YTAPHRVLAT AYTGTTTYTA SARGDLAHLT TTHARHLPTS FNFGAVKAET ITELLVRMKR

 AELYCPRPIL PIQPTGDRHK QPLVAPAKQL LGIPSKGEEL FTGVVPILVE LDGDVNGHKF

 SVRGEGEGDA TNGKLTLKFI CTTGKLPVPW PTLVTTLSHG VQCFARYPDH MKQHDFFKSA

 MPEGYVQERT IFFKDDGTYK TRAEVKFEGD TLVNRIELKG VDFKEDGNIL GHKLEYNFNS

 HNIYIMAVKQ KNGIKVNFKI RHNVEDGSVQ LADHYQQNTP IGDGPVLLPD SHYLSTQSVL

 SKDPNEKRDH MVLLEFRTAA GITLGMDELY KHHHHHH

Orange: VP1 PDB: 1QGC\_1

Blue: EBFP2

<https://www.genome.jp/tools-bin/clustalw>

[clustalw.aln](https://www.genome.jp/tools-bin/pushfile?190617154834vf3J4+clustalw.aln)

CLUSTAL 2.1 multiple sequence alignment

GFP ENLYFQGSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLP

EBFP -------SKGEELFTGVVPILVELDGDVNGHKFSVRGEGEGDATNGKLTLKFICTTGKLP

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GFP VPWPTLVTTLTYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTISFKDDGNYKTRAEVKF

EBFP VPWPTLVTTLSHGVQCFARYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGTYKTRAEVKF

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GFP EGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYITADKQKNGIKANFKIRHNIEDG

EBFP EGDTLVNRIELKGVDFKEDGNILGHKLEYNFNSHNIYIMAVKQKNGIKVNFKIRHNVEDG

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GFP SVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMD

EBFP SVQLADHYQQNTPIGDGPVLLPDSHYLSTQSVLSKDPNEKRDHMVLLEFRTAAGITLGMD

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GFP ELY

EBFP ELY

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EBFP 3D structure using Swiss Model

